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RAW SEQUENCE LISTING DATE: 06/18/2003
PATENT APPLICATION: **US/09/828,574A** TIME: 11:45:18

Input Set : **A:\UCSD1310-1.ST25.txt**
Output Set: **N:\CRF4\06182003\I828574A.raw**

ENTERED

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<110> APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
      ALBANI, Salvatore
      PRAKKEN, Berent J.
<120> TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
<130> FILE REFERENCE: UCSD1310-1
<140> CURRENT APPLICATION NUMBER: US 09/828,574A
<141> CURRENT FILING DATE: 2001-04-06
<150> PRIOR APPLICATION NUMBER: US 60/224,104
<151> PRIOR FILING DATE: 2000-08-09
<160> NUMBER OF SEQ ID NOS: 23
<170> SOFTWARE: PatentIn version 3.1
<210> SEQ ID NO: 1
<211> LENGTH: 573
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
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            20                  25                  30
Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
        35                  40                  45
Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
    50                  55                  60
Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
65                  70                  75                  80
Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
                85                  90                  95
Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly
            100                 105                 110
Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe
        115                 120                 125
Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
    130                 135                 140
Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
145                 150                 155                 160
Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
                165                 170                 175
Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
            180                 185                 190
Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
        195                 200                 205
Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
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81     210                 215                 220
84 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
85 225                 230                 235                 240
88 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
89                 245                 250                 255
92 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
93             260                 265                 270
96 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
97         275                 280                 285
100 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
101     290                 295                 300
104 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
105 305                 310                 315                 320
108 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
109                 325                 330                 335
112 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
113             340                 345                 350
116 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu
117         355                 360                 365
120 Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
121     370                 375                 380
124 Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
125 385                 390                 395                 400
128 Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
129                 405                 410                 415
132 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
133             420                 425                 430
136 Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile
137         435                 440                 445
140 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
141     450                 455                 460
144 Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
145 465                 470                 475                 480
148 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
149                 485                 490                 495
152 Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
153             500                 505                 510
156 Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
157         515                 520                 525
160 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
161     530                 535                 540
164 Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
165 545                 550                 555                 560
168 Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
169                 565                 570
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 15
174 <212> TYPE: PRT
175 <213> ORGANISM: Mycobacterium
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183 <210> SEQ ID NO: 3
184 <211> LENGTH: 15
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
188 <400> SEQUENCE: 3
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191 1               5                   10                  15
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 15
196 <212> TYPE: PRT
197 <213> ORGANISM: Mycobacterium
199 <400> SEQUENCE: 4
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202 1               5                   10                  15
205 <210> SEQ ID NO: 5
206 <211> LENGTH: 15
207 <212> TYPE: PRT
208 <213> ORGANISM: Homo sapiens
210 <400> SEQUENCE: 5
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213 1               5                   10                  15
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 15
218 <212> TYPE: PRT
219 <213> ORGANISM: Mycobacterium
221 <400> SEQUENCE: 6
223 Glu Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys
224 1               5                   10                  15
227 <210> SEQ ID NO: 7
228 <211> LENGTH: 15
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
232 <400> SEQUENCE: 7
234 Lys Cys Glu Phe Gln Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys
235 1               5                   10                  15
238 <210> SEQ ID NO: 8
239 <211> LENGTH: 15
240 <212> TYPE: PRT
241 <213> ORGANISM: Mycobacterium
243 <400> SEQUENCE: 8
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246 1               5                   10                  15
249 <210> SEQ ID NO: 9
250 <211> LENGTH: 15
251 <212> TYPE: PRT
252 <213> ORGANISM: Homo sapiens
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     261 <211> LENGTH: 15
     262 <212> TYPE: PRT
     263 <213> ORGANISM: Artificial sequence
     265 <220> FEATURE:
     266 <223> OTHER INFORMATION: dnaJP1 peptide
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     271 1               5                   10                  15
     274 <210> SEQ ID NO: 11
     275 <211> LENGTH: 15
     276 <212> TYPE: PRT
     277 <213> ORGANISM: Artificial sequence
     279 <220> FEATURE:
     280 <223> OTHER INFORMATION: Irrelevant dnaJpV peptide
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     285 1               5                   10                  15
     288 <210> SEQ ID NO: 12
     289 <211> LENGTH: 11
     290 <212> TYPE: PRT
     291 <213> ORGANISM: Artificial sequence
     293 <220> FEATURE:
     294 <223> OTHER INFORMATION: pan-DR binder peptide
     296 <220> FEATURE:
     297 <221> NAME/KEY: MISC_FEATURE
     298 <222> LOCATION: (2)..(2)
     299 <223> OTHER INFORMATION: Xaa is any amino acid
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     305 1               5                   10
     308 <210> SEQ ID NO: 13
     309 <211> LENGTH: 573
     310 <212> TYPE: PRT
     311 <213> ORGANISM: Homo sapiens
     313 <400> SEQUENCE: 13
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     316 1               5                   10                  15
     319 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
     320             20                  25                  30
     323 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
     324         35                  40                  45
     327 Asp Ala Val Ala Val Thr Met Glu Pro Lys Gly Arg Thr Val Ile Ile
     328     50                  55                  60
     331 Glu Gln Ser Trp Gly Ser Pro Asn Val Thr Lys Asp Gly Val Thr Val
     332 65                  70                  75                  80
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```
335 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
336                 85                  90                  95
339 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ser Gly Asp Gly
340             100                 105                 110
343 Thr Thr Thr Ala Thr Val Leu Ala Gly Ser Ile Ala Lys Glu Gly Phe
344         115                 120                 125
347 Gln Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
348     130                 135                 140
351 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
352 145                 150                 155                 160
355 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Met Ile Ser Ala
356                 165                 170                 175
359 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
360             180                 185                 190
363 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
364         195                 200                 205
367 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
368     210                 215                 220
371 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
372 225                 230                 235                 240
375 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Val Gln Ser
376                 245                 250                 255
379 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His His Lys Pro Leu Val
380             260                 265                 270
383 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Ile Leu
384         275                 280                 285
387 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
388     290                 295                 300
391 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
392 305                 310                 315                 320
395 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
396                 325                 330                 335
399 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
400             340                 345                 350
403 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Leu Glu
404         355                 360                 365
407 Lys Arg Ile Gln Glu Ile Ile Gly Gln Leu Asp Val Thr Thr Ser Glu
408     370                 375                 380
411 Tyr Glu Lys Glu Lys Leu Asn Glu Trp Leu Ala Lys Leu Ser Asp Gly
412 385                 390                 395                 400
415 Val Val Val Leu Lys Phe Gly Gly Thr Ser Asp Val Glu Val Asn Glu
416                 405                 410                 415
419 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
420             420                 425                 430
423 Glu Gly Gly Ile Val Leu Gly Gly Gly Phe Ala Leu Leu Arg Cys Ile
424         435                 440                 445
427 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
428     450                 455                 460
431 Met Glu Ile Val Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Thr Ala
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; Xaa Pos. 2